

Figure 1

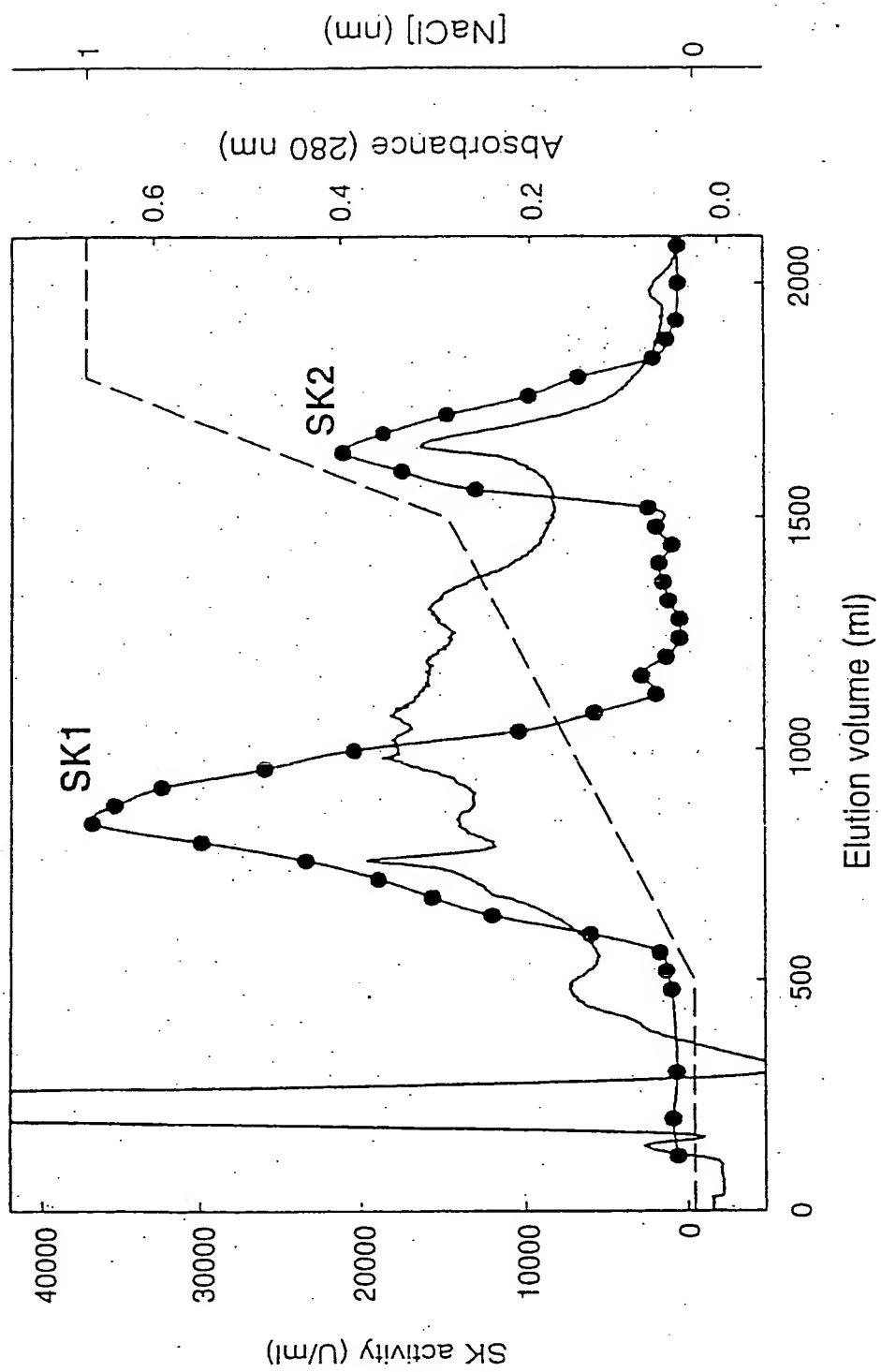
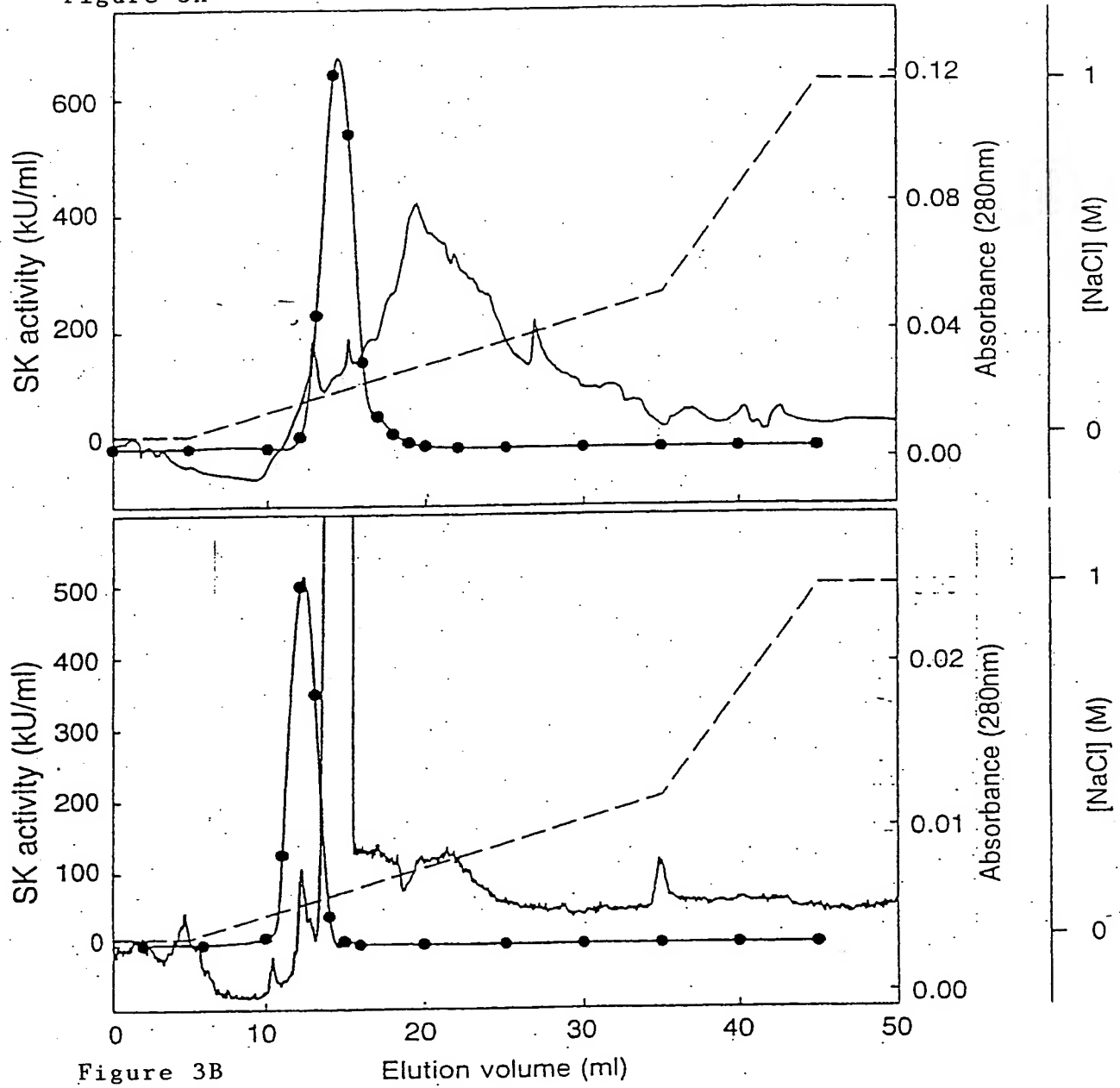


Figure 2

Figure 3A



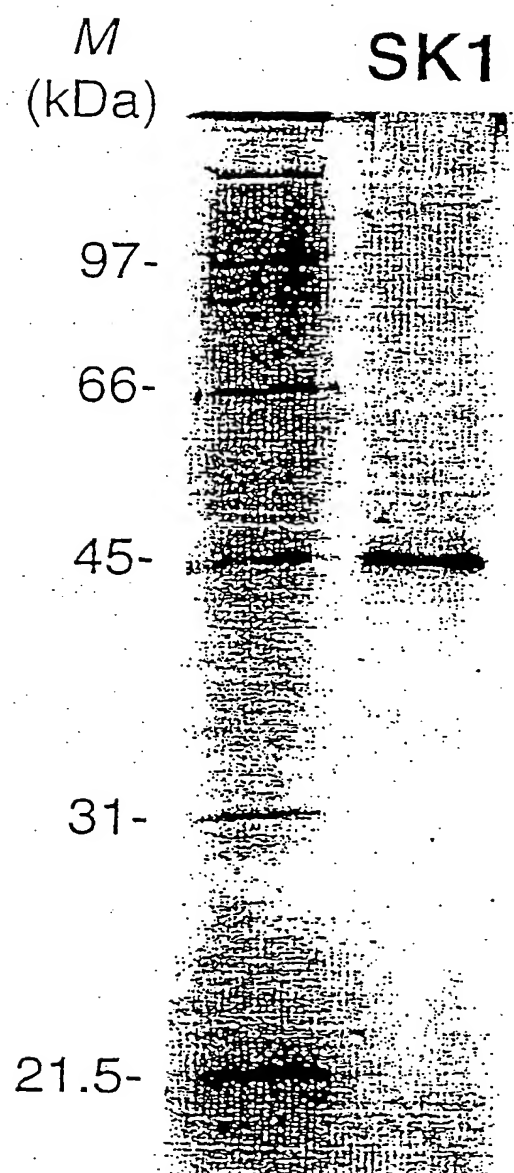


Figure 4

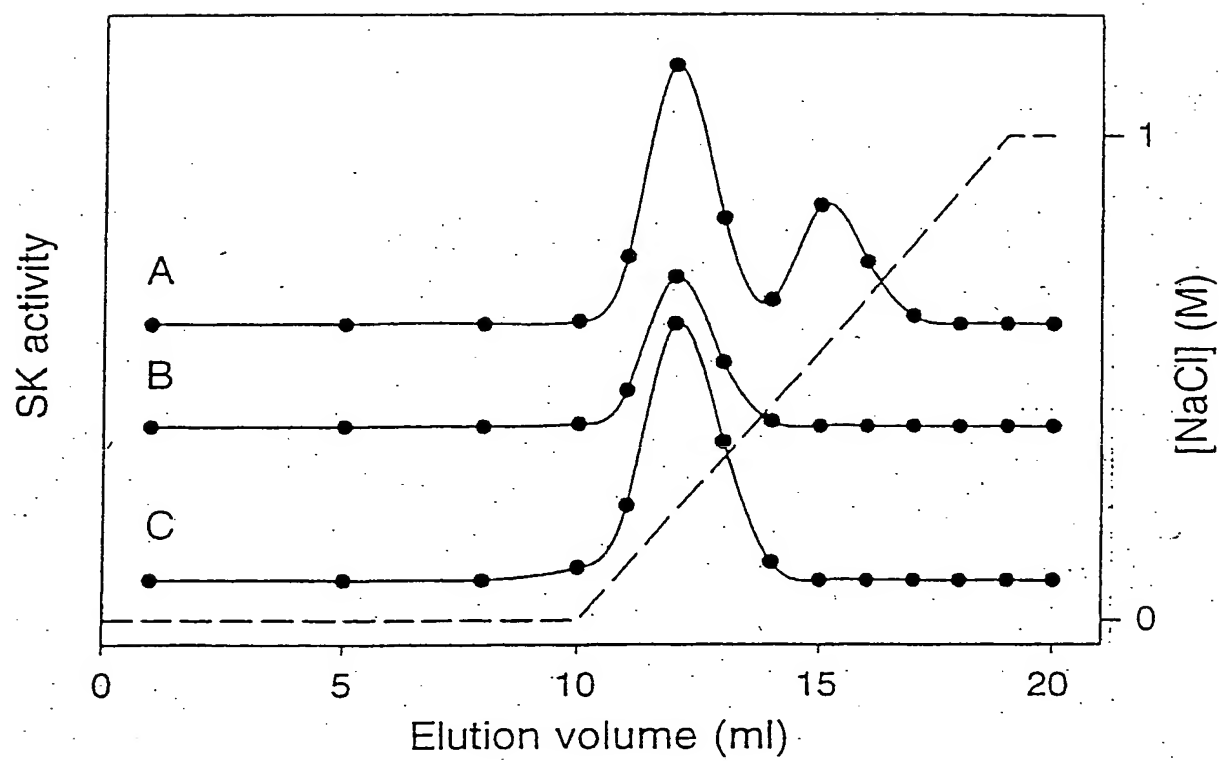


Figure 5

Cloning of HUVEC SK

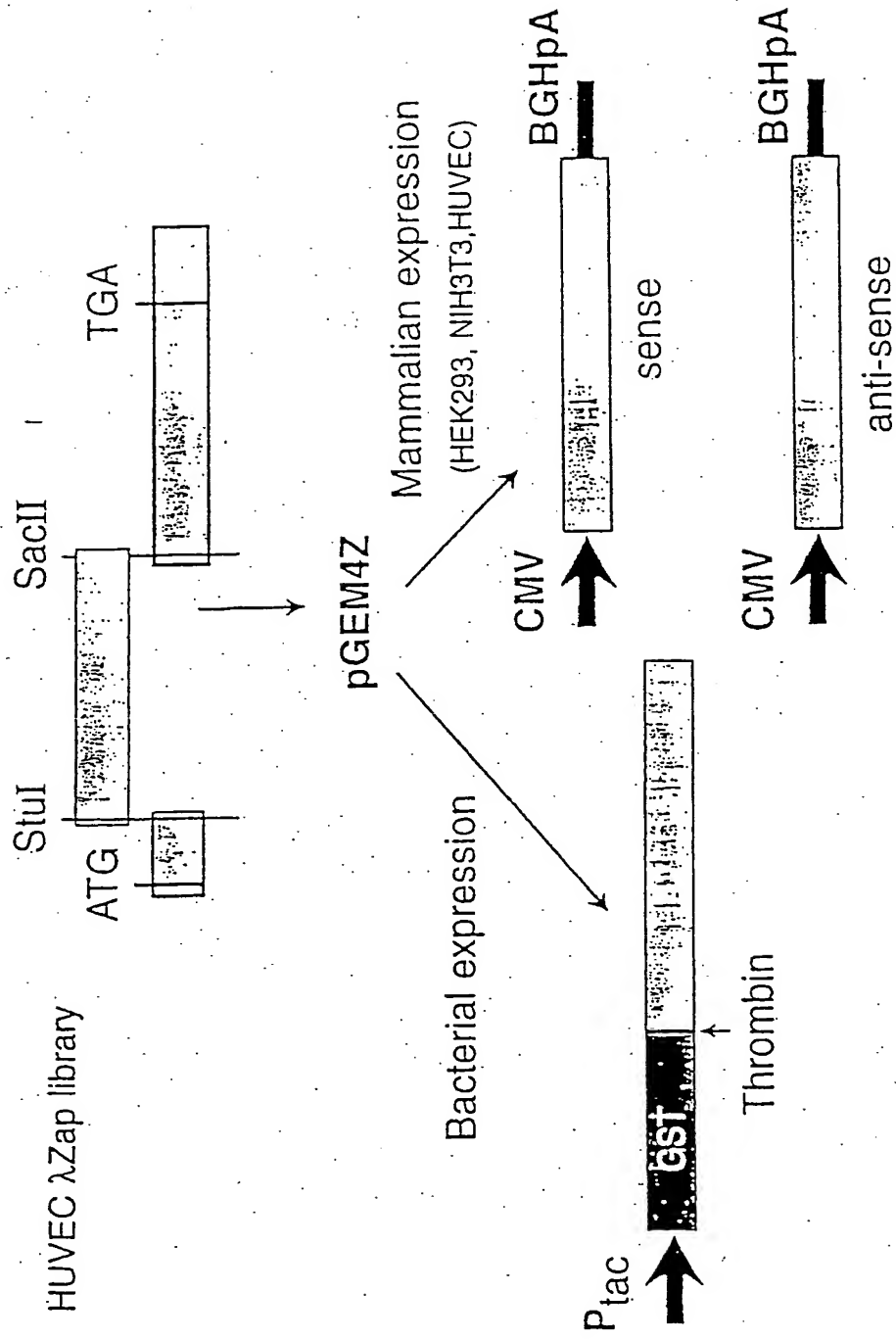


Figure 6

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1      M D P A G G P R G V L P R P C R V L V      19
1 gagcgcgggtcagggttATGGATCCAGCGGGCGGGCGGTGCTCCCGCGGCGCTGCCGGTGGTG      75

20 L L N P R G G K A L Q L F R S H V Q P L L A E      44
76 CTGCTGAACCCGCGGGCAAGGCCCTTGCAAGCTCTCCGGAGTCACGTGCAGCCCCCTTTGGCTGAG      150

45 A E I S F T L M L T E R R N H A R E L V R S E E L      69
151 GCTGAAATCTCCTTCACGCTGATGCTCACTGAGCGGGGGAACCAAGCGGGGAGCTGGTGGGTCGGAGGAGCTG      225

70 G R W D A L V V M S G D G L M H E V V N G L M E R      94
226 GGCCGCTGGGACGCTCTGGTGGTCATGTCTGGAGACGGGCTGATGCACGAGGTGGTGAACGGGCTCATGGAGCGG      300

95 P D W E T A I Q K P L C S L P A G S G N A L A A S      119
301 CCTGACTGGGAGACCGCCATCCAGAAGCCCCCTGTGTAGCCTCCAGCAGGCTCTGGCAACGGCTGGCAGCTTCC      375

120 L N H Y A G Y E Q V T N E D L L T N C T L L L C R      144
376 TTGAACCATTAATGCTGGCTATGAGCAGGTACCAATGAAGACCTCCTGACCAACTGCACGCTATTGCTGTGCCCG      450

145 R L L S P M N L L S L H T A S G L R L F S V L S L      169
451 CGGCTGCTGTACCCCATGAACCTGCTGTCTCTGCACACGGCTTCGGGGCTGCCCTCTCTGTGCTCAGCCTG      525

170 A W G F I A D V D L E S E K Y R R L G E M R F T L      194
526 GCCTGGGGCTTCATTGCTGATGTGGACCTAGAGAGTGAGAAAGTATCGGCGTCTGGGGGAGATGCCGCTTCACTCTG      600

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Figure 7A-1

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195 G T F L R L A A L R T Y R G R L A Y L P V G R V G 219
601 GGCACCTTCCCTGCGTCTGGCAGCCTTGGCAGCCTTACCGGGCCGACTGGCTTACCTCCCTGTAGGAAGAGTGGGT 675

220 S K T P A S P V V V Q Q G P V D A H L V P L E E P 244
676 TCCAAGACACCTGCCTCCCCCGTTGTGGTCCAGCAGGGCCCGGTAGATGCACACCTTGTGCCACTGGAGGAGCCA 750

245 V P S H W T V V P D E D F V L V L A L L H S H L G 269
751 GTGCCCCCTCACTGGACAGTGGTGCCCGACGAGGACTTGTGCTAGTCTCTGGCACTGCTGCACCTCGCACCTGGGC 825

270 S E M F A A P M G R C A A G V M H L F Y V R A G V 294
826 AGTGAGATGTTGTGTGCACCCATGGCCCGCTGTGCAGCTGGCGTCATGCATCTGTCTACGTGCGGGCGGGAGTG 900

295 S R A M L L R L F L A M E K G R H M E Y E C P Y L 319
901 TCTCGTGCCATGCTGCTGGCCCTCTTCCCTGGCCATGGAGAAGGCAGGCATATGGAGTATGAATGCCCCCTACTTG 975

320 V Y V P V V A F R L E P K D G K G M F A V D G E L 344
976 GTATATGTGCCCGTGGTCCGCTTCCGCTTGGAGCCCAAGGATGGGAAAGGTATGTTTGCAGTGGATGGGGAATTG 1050

345 M V S E A V Q G Q V H P N Y F W M V S G C V E P P 369
1051 ATGGTTAGCGAGGCCCGTGCAGGGCCAGGTGCACCCCAACTACTTCTGGATGGTCAGCGGTTGCGTGGAGCCCCCG 1125

370 P S W K P Q Q M P P P E E P L . 384
1126 CCCAGCTGGAAGCCCCCAGCAGATGCCACCGCCAGAAAGCCCCCTTatga 1173

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Figure 7A-2

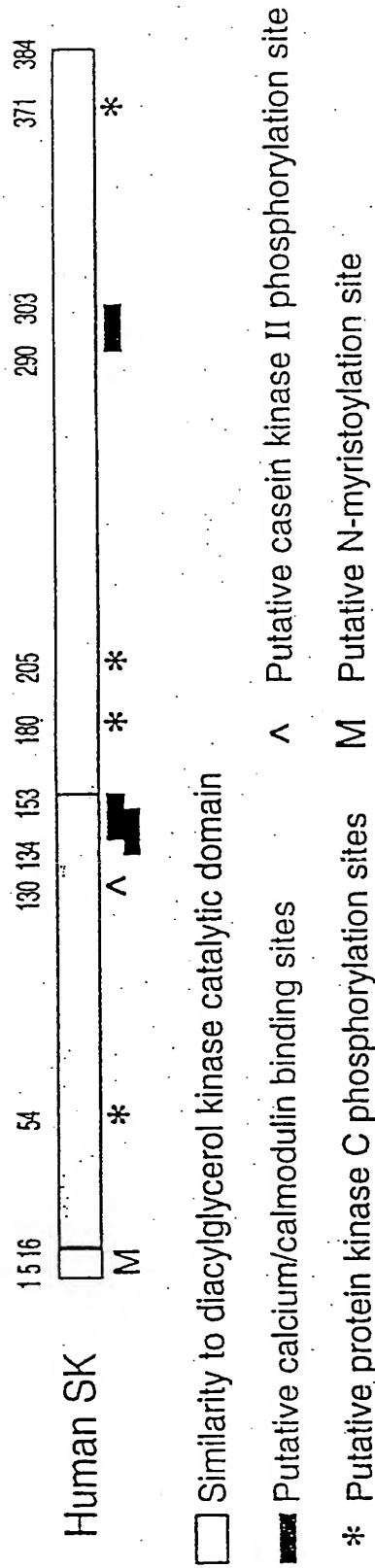
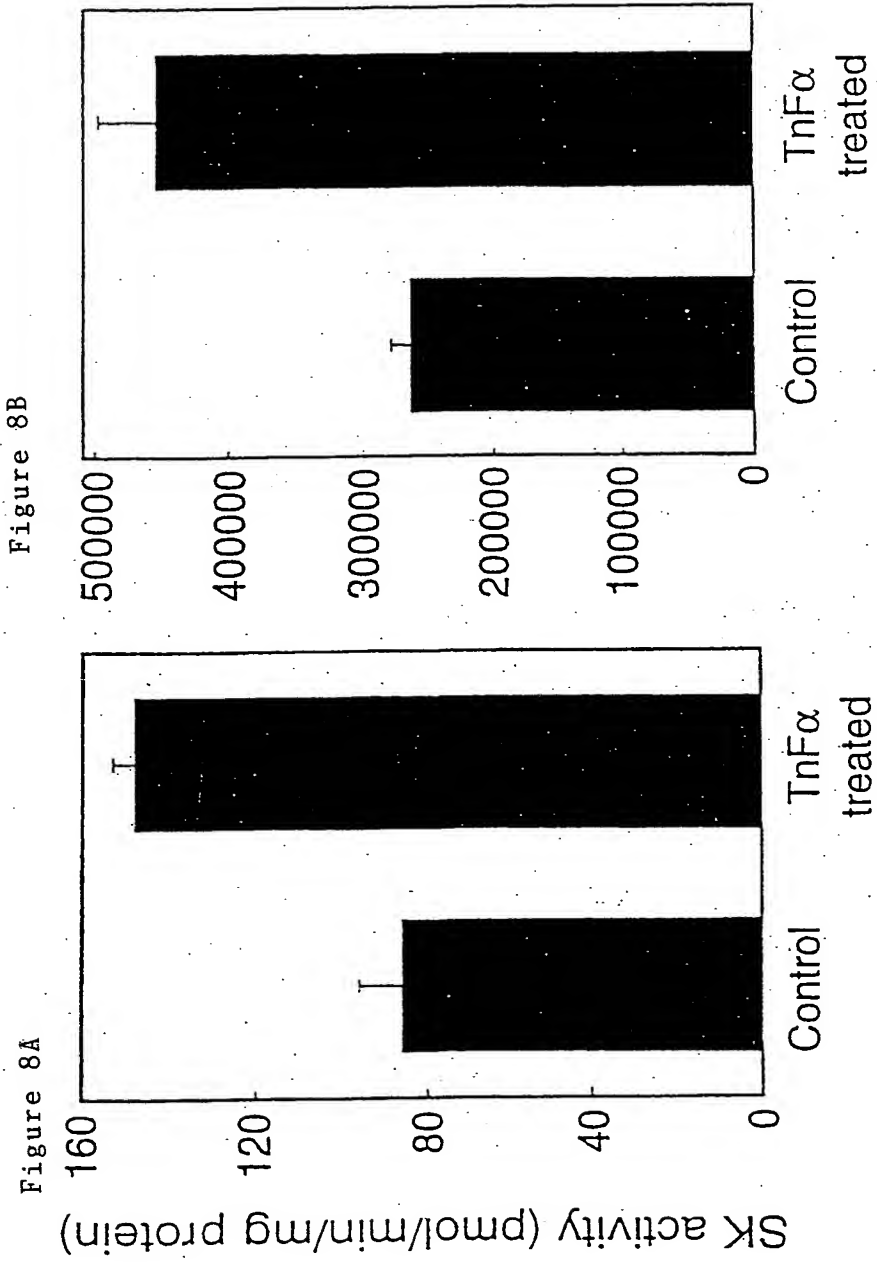


Figure 7B



hSK	1MDPAGGPRGVLP	PCRVLV	LLNPR	GGKGK ALQL	FR SHVQ PL	LAEA	EIS
mSK1a	1MEPECPRGLLP	PCRVLV	LLNPQ	GGKGK ALQL	FQ SRVQ PF	EEAE	IT
mSK1b	1	MWCCVL	FVVECP	RGLLP	PCRVLV	LLNPQ	GGKGK ALQL	FQ SRVQ PF EEAEIT
Yeast LCB4	206	NISSGT	VEEILE	KSYEN	SKRNR	SILV	IINPH	GGKGK TAKNL FL TKAR PI LVESGCK
Yeast LCB5	252	DL...	VEEIL	KRSYK	NRNKS	SIFV	IINPF	GGKGK AKKL EM TKAK PL LASRCS
S: pombe	90FCEYLL	DVAYK	GIGIK	RSRRF	VF	INPH	GGKGK AKHWESEAE PF VSSAHSI
C. elegans	63	ENEQLTS	VILSR	KPPPE	QCRC	GNLL	VFINP	NS GTGK SL ET FANTV GP K LD DKSLIR
Consensus	*R	...*	*V	*NP	GGKGK	...*F*...P.L.*
hSK	112	SGNA LAAS	LNHYAG	YEQVT	NEDLL	TNCT	LLCRR	...LLSPMNL
mSK1a	111	SGNA LAAS	SVNHYAG	YEQVT	NEDLL	INCT	LLCRR	...RLSPMNL
mSK1b	118	SGNA LAAS	SVNHYAG	YEQVT	NEDLL	INCT	LLCRR	...RLSPMNL
Yeast LCB4	325	SGNA MSIS	CHWTN	NPSYAA	CLVK	SIETR	IDL
Yeast LCB5	368	SGNA MSVS	CHWTN	NPSYST	CLIK	SIETR	IDL
S: pombe	203	SGNA AFSYN	ATGQL	KPALTA	LEIL	KGRPT	SFDL
C. elegans	184	SGNGL LC	SV	LSKYG	TKMNEK	SVMERAL	EIATS	PTAKAES
Consensus		SGNA*	...S*	*L	*M*M

Figure 9A

hSK	211AYLP.....	VGRVGSKTPASPVVVQQGPVD
mSK1a	210AYLP.....	VGTVASKRPAST.LVQKGPVD
mSK1b	217AYLP.....	VGTVASKRPAST.LVQKGPVD
Yeast LCB4	435	ENKDKNKGCLTFP...	NPSNSSPDLLSKNNINNSTKDE.....
Yeast LCB5	478	EH...KNKGSLEFQHI	TMNKDNEDCDNYNYENEYETENEDEDADDEDSDLIS
S. pombe	308	EKSKNLAPMSESSDSK.....
C. elegans	284TYRPPYKPKGFHPSSNVFSVYEKTTQQR	IDDSKVKTNGSVSDSEETME
Consensus	**
hSK	282	AGVMHLFYV..RAGVSR	AMLLRLFLAMEKGRHMEYEC
mSK1a	280	AGVMHLFYV..RAGVSR	AALLRLFLAMQKGKHMELDC
mSK1b	287	AGVMHLFYV..RAGVSR	AALLRLFLAMQKGKHMELDC
Yeast LCB4	532	DGTIDLVI	TDARIPVTR..MTPILLSLDKGS
Yeast LCB5	586	DGTMDMVI	TDARTSLTR..MAPILLGLDKGS
S. pombe	367	DGLIDVVI	VYSKQFRKS..LLSMFTQLDN
C. elegans	388	DNRHLSYILWKDIGTR	VNI
Consensus		G.*.....*	*R...*.L**..G.H.....P.*...*.P..

Figure 9B

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FTLMLTERRNHARE.LVRSEELGRWDALVVMSGDGLMHEVVNGLMERPDWETAI.QKPLCSLPAG
FKLILTERKNHARE.LVCAEELGHWDALAVMSGDGLMHEVVNGLMERPDWETAI.QKPLCSLPGG
FKLILTERKNHARE.LVCAEELGHWDALAVMSGDGLMHEVVNGLMERPDWETAI.QKPLCSLPGG
IEIAYTKYARHAID.IAKDLDISKYDTIACASSGDGIPIYEVINGLYRRPDRVDAFNKLAVTQLPCG
IEVYTKYPGHAIE.IAREMDIDKYDTIACASSGDGIPHEVINGLYQRPDHVKAFNNIAITEIPCG
CEVLTTRRKDHAKS.IAKNLDVGSYDGILSVGGDGLFHEVINGLGERDDYLEAF.KLPVCMIPGG
YEVVVTGPNHARNVLMTKADLGKFNGLVILSGDGLVFEALNGILCREDAFRIFPTLPIGIVPSG
...T....HA.*.*.*.*D.*.*SGDG*.EV*NGL..R.D...A...*.*P.G

FVLSLAWGFIAADVDLESEKYRR.LGEMRFTLGTFLRLAALRTYRGRL.....
YSVLSLSWGFVADVDLESEKYRR.LGEIRFTVGTFFRLASLRIYQQQL.....
YSVLSLSWGFVADVDLESEKYRR.LGEIRFTVGTFFRLASLRIYQQQL.....
LSFLSQTYGVIAESDINTE.FIRWMGPVRFNLGVAFNIIQGKKYPCEVFVKYAAKSKKELKVHFL
LSFLSQTYGLIAETDINTE.FIRWMGPARFELGVAFNIIQKKKYPCEIYVKYAAKSKNELKNHYL
YSFLTANYGIIADCDIGTE.NWRFMGENRAYLGFFLRLFQKPDWKCSIEMDVVSSDRTEIKHMY.
ASFLSIGWGLMADIDIDSEKWRKSLGHHRFTVMGFIRSCNLSRYKGRL.....
.S.LS.**G.*A*.D***E.*R.*G..RF.*G.....*Y...*.....

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Figure 9C

Figure 9D

Figure 10A

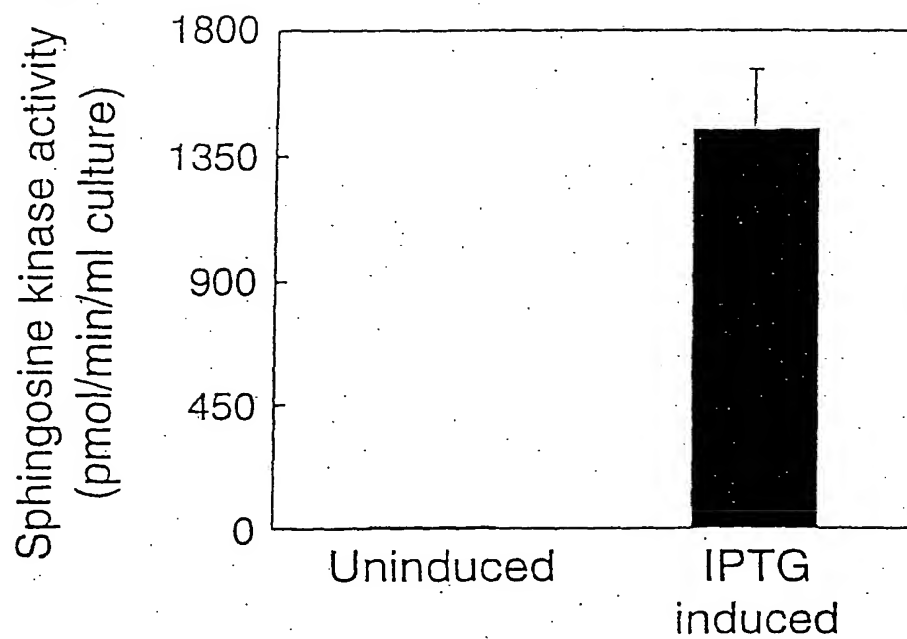


Figure 10B

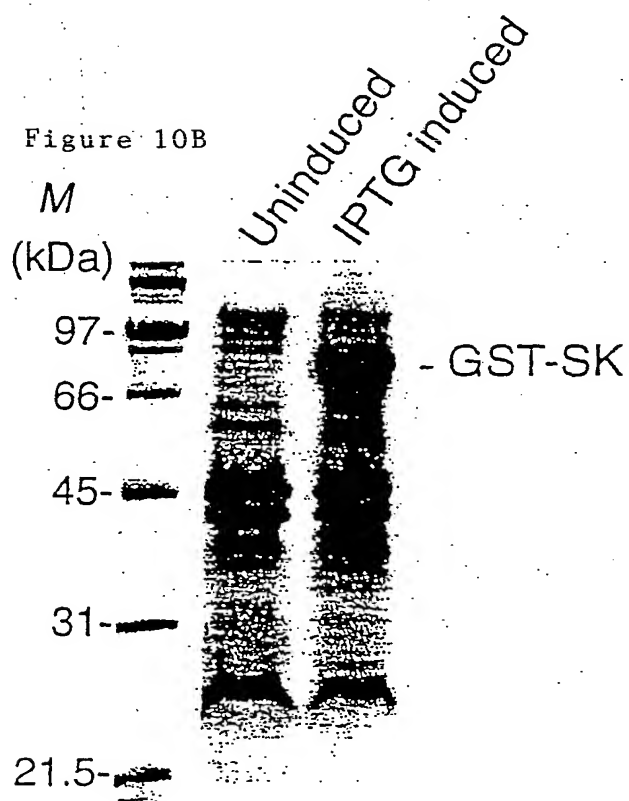
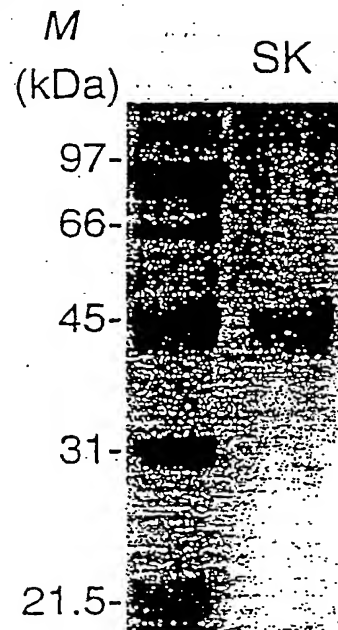


Figure 10C



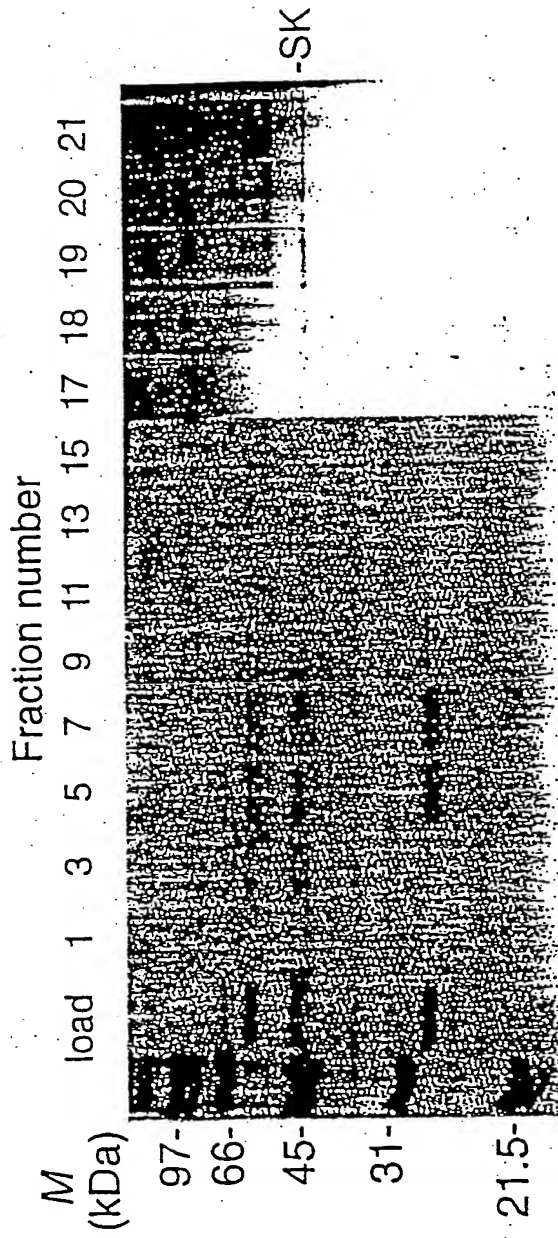


Figure 11A

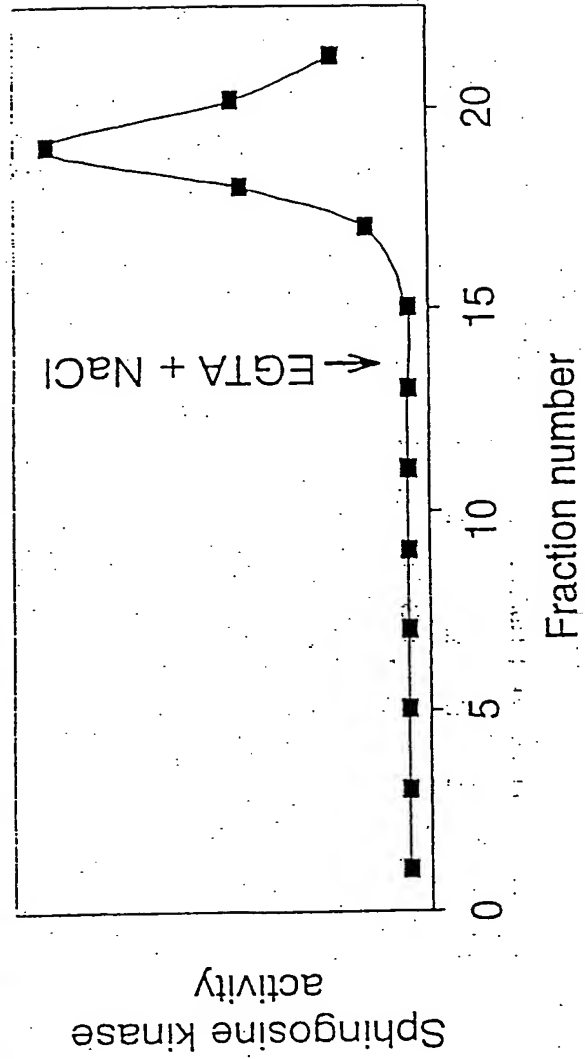


Figure 11B

Figure 12A

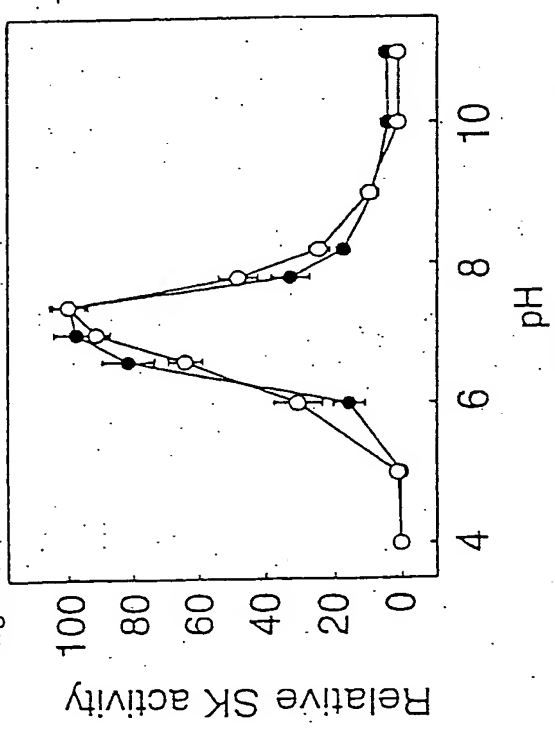


Figure 12B

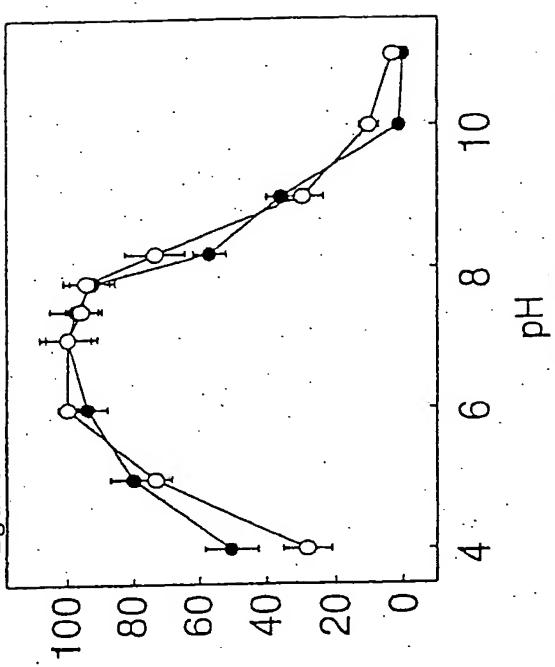


Figure 12C

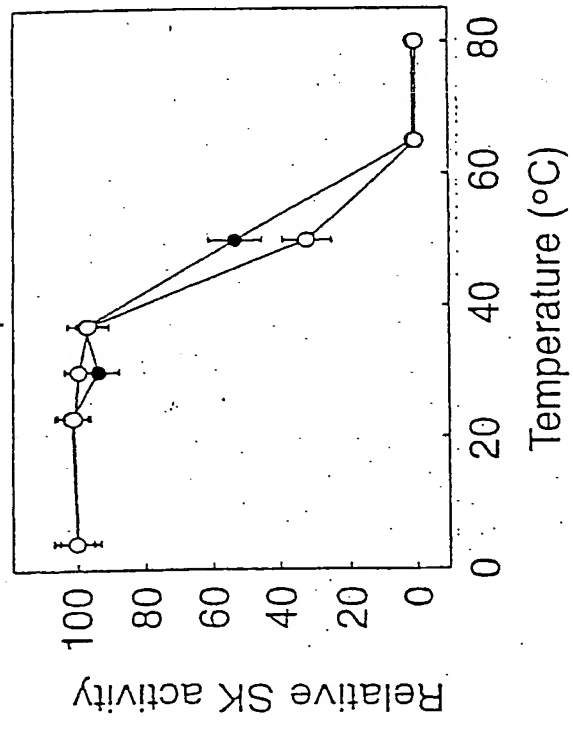
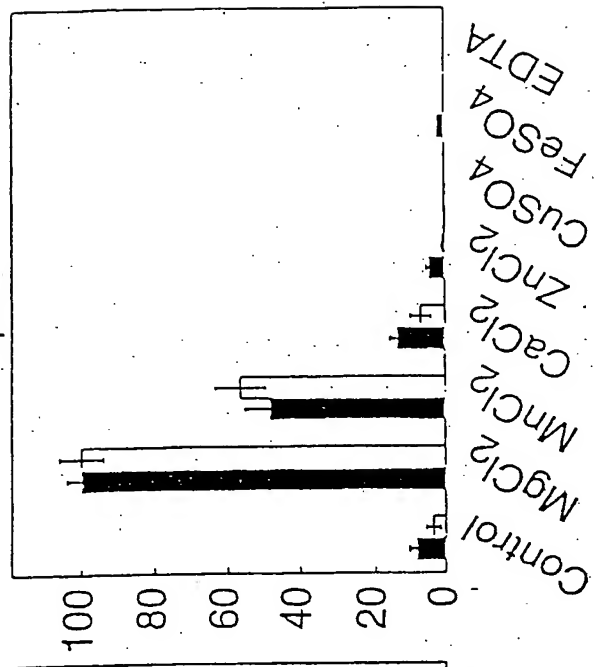
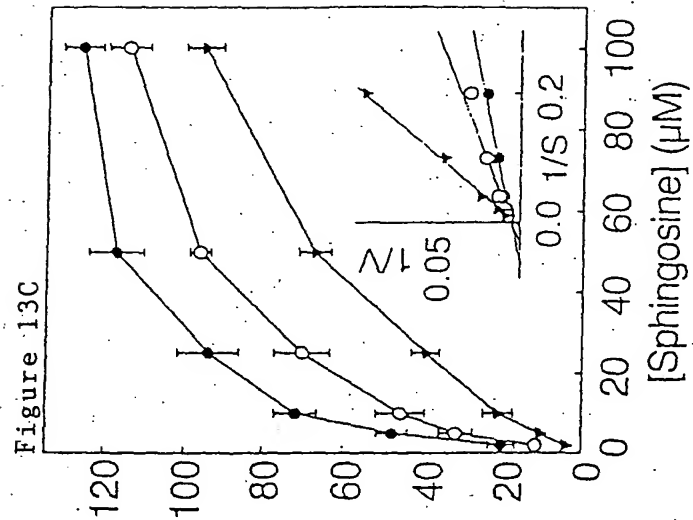
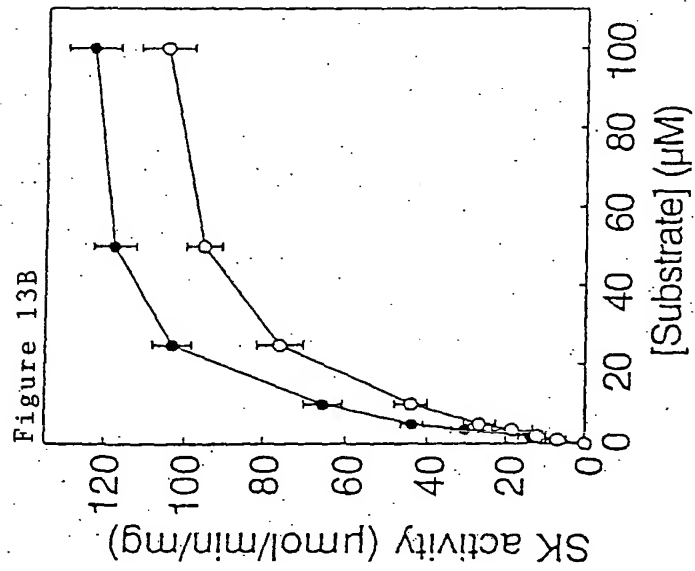
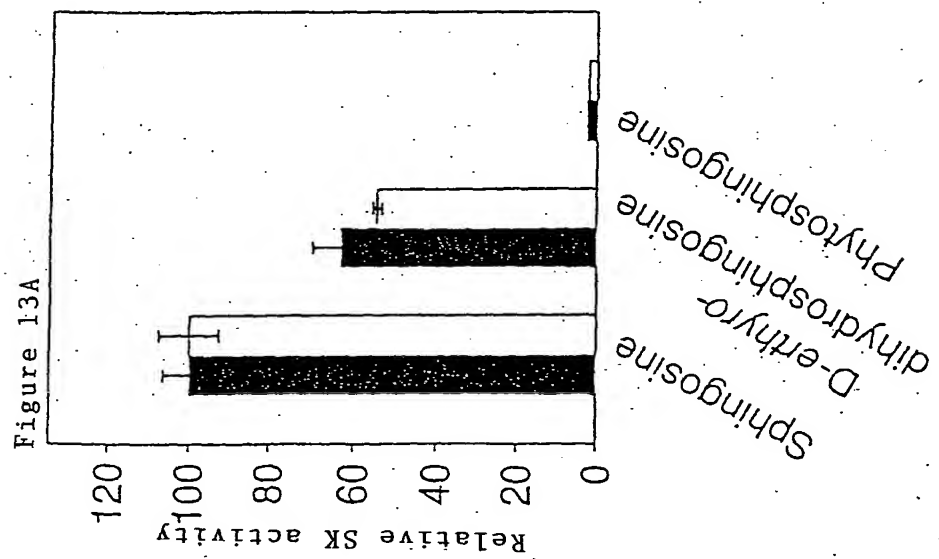


Figure 12D





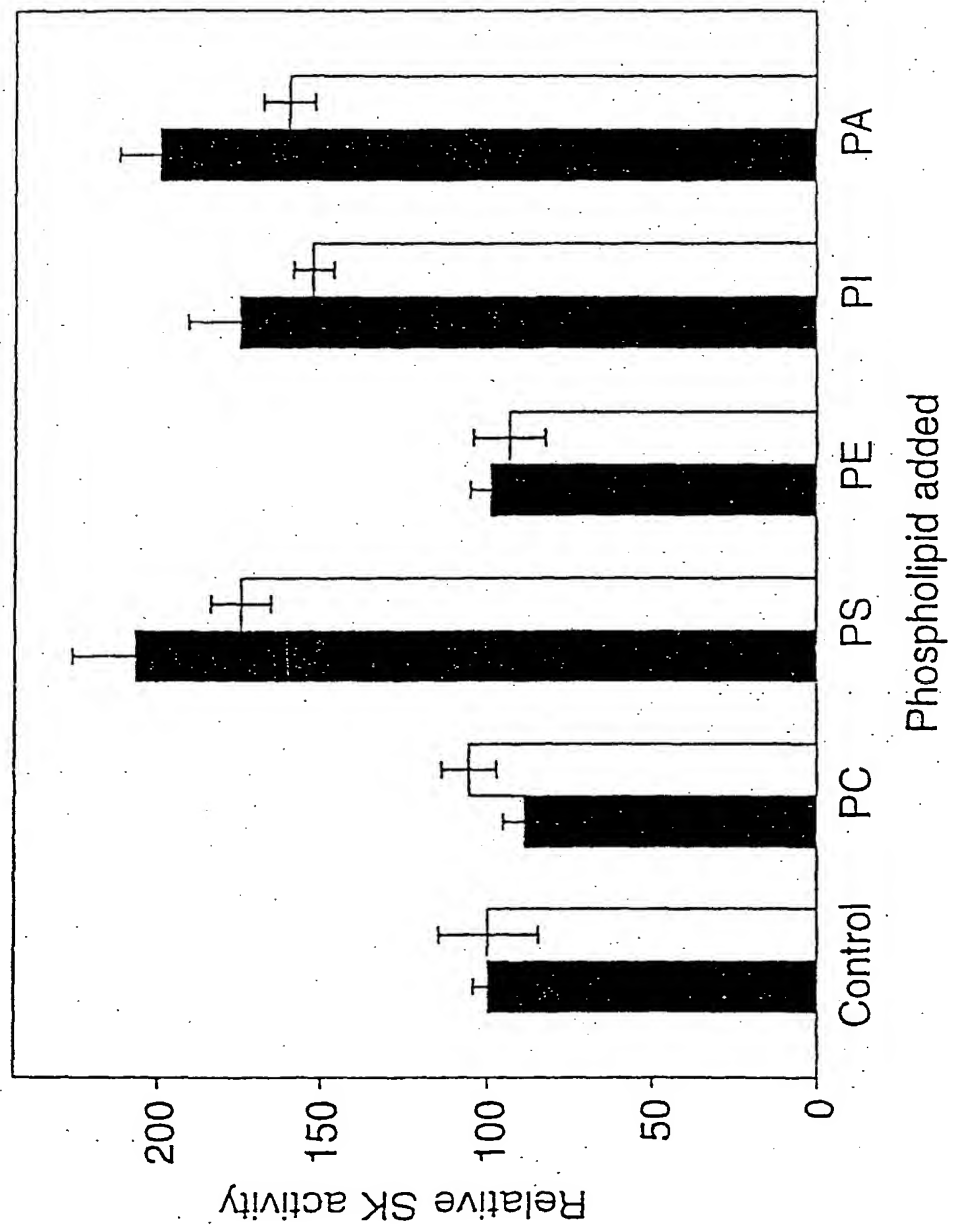


Figure 14